GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:19 ; Search time 8498.8 Seconds
(without alignments)
31.610 Million cell updates/sec

Title: US-09-851-670-12
Perfect score: 25
Sequence: 1 acagctcgcccccattaacatattc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	13.4	53.6	33	13	TA80C11Q	AL461346 T. brucei
c	2	13.4	53.6	50	10	AU103898	AU103898 AU103898
c	3	13	52.0	50	10	AU107252	AU107252 AU107252
	4	13	52.0	52	11	W71856	W71856 me45f07.r1
	5	13	52.0	52	11	BF643572	BF643572 NF057E06E
	6	13	52.0	52	13	TA235H01P	AL481430 T. brucei
	7	12.8	51.2	49	10	AI723111	AI723111 fc25g02.y
	8	12.8	51.2	50	10	AU107456	AU107456 AU107456
c	9	12.8	51.2	52	10	AA190304	AA190304 mt94h01.r
c	10	12.6	50.4	30	13	AZ662142	AZ662142 1M0541M03
c	11	12.6	50.4	49	10	AA857265	AA857265 of75f01.s
c	12	12.6	50.4	50	10	AU102605	AU102605 AU102605
c	13	12.6	50.4	50	10	AU104819	AU104819 AU104819
c	14	12.6	50.4	60	13	AZ460727	AZ460727 1M0266O11
	15	12.4	49.6	36	13	AZ331596	AZ331596 1M0059E08
	16	12.4	49.6	55	11	BG152186	BG152186 nag73g01.
	17	12.4	49.6	57	13	AZ648926	AZ648926 1M0518G23
c	18	12.2	48.8	28	13	TA380E12Q	AL497833 T. brucei
c	19	12.2	48.8	39	13	AZ986277	AZ986277 2M0268J20
	20	12.2	48.8	40	10	AA588339	AA588339 nm93b07.s
c	21	12.2	48.8	40	13	AZ665717	AZ665717 1M0547L15
c	22	12.2	48.8	50	10	AU102603	AU102603 AU102603
c	23	12.2	48.8	50	10	AU104015	AU104015 AU104015
c	24	12.2	48.8	50	10	AU104017	AU104017 AU104017
c	25	12.2	48.8	51	13	TA289F12Q	AL486591 T. brucei
c	26	12.2	48.8	53	13	B36066	B36066 HS-1031-B1-
	27	12.2	48.8	58	10	AI499235	AI499235 to08g07.x
c	28	12.2	48.8	59	10	AI954847	AI954847 wx90a10.x
	29	12	48.0	28	13	AZ485440	AZ485440 1M0312B22
	30	12	48.0	31	11	C01612	C01612 HUMGS000862
c	31	12	48.0	41	13	AZ484492	AZ484492 1M0311A04
c	32	12	48.0	45	13	AZ814934	AZ814934 2M0082G22
c	33	12	48.0	50	13	AZ659610	AZ659610 1M0537P02
	34	12	48.0	50	13	AZ918083	AZ918083 1006003B0
c	35	12	48.0	53	13	AZ807379	AZ807379 2M0070M08
c	36	12	48.0	54	10	AA855787	AA855787 vw74h03.r
	37	12	48.0	54	13	B03584	B03584 cSRL-182F5-
c	38	12	48.0	54	13	TA374D02P	AL495664 T. brucei
	39	12	48.0	57	13	AZ450809	AZ450809 1M0249P10
c	40	12	48.0	58	11	N28963	N28963 yx39c08.r1
c	41	12	48.0	59	10	AI337657	AI337657 qw91e11.x
c	42	11.8	47.2	23	13	AZ339893	AZ339893 1M0071M03
	43	11.8	47.2	39	13	AZ333190	AZ333190 1M0062F08
	44	11.8	47.2	43	10	AI461342	AI461342 fb43d04.x
c	45	11.8	47.2	49	13	AZ810303	AZ810303 2M0074E18

ALIGNMENTS

RESULT 1
TA80C11Q/c
LOCUS TA80C11Q 33 bp DNA GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 80c11, reverse sequence, genomic survey sequence.
ACCESSION AL461346
VERSION AL461346.1 GI:11860628
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .33

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                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="80c11"
BASE COUNT         6 a      7 c     10 g     10 t
ORIGIN


  Query Match             53.6%;  Score 13.4;  DB 13;  Length 33;
  Best Local Similarity   73.9%;  Pred. No. 4.6e+04;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2 cagctcgccccccattaacatatt 24
           |||||||| || | | ||| | |
Db      26 CAGCTCGCTCCAACTGACACAGT 4


RESULT   2
AU103898/c
LOCUS       AU103898        50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU103898 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT01668, mRNA sequence.
ACCESSION   AU103898
VERSION     AU103898.1  GI:13553419
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT01668"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT        11 a     11 c     20 g      8 t
ORIGIN


  Query Match             53.6%;  Score 13.4;  DB 10;  Length 50;
  Best Local Similarity   93.3%;  Pred. No. 4.9e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 cagctcgcccccatt 16
           |||||||||||||| |
Db      38 CAGCTCGCCCCCAGT 24


RESULT   3
AU107252/c
LOCUS       AU107252        50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU107252 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            LNG08445, mRNA sequence.
ACCESSION   AU107252
VERSION     AU107252.1  GI:13556773
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="LNG08445"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT        18 a      9 c     16 g      7 t
ORIGIN


  Query Match             52.0%;  Score 13;  DB 10;  Length 50;
  Best Local Similarity   76.2%;  Pred. No. 7.3e+04;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       5 ctcgccccccattaacatattc 25
           || | |||||||||||  | |
Db      43 CTGGGCCCCCATTAACACGTCC 23


RESULT   4
W71856
LOCUS       W71856          52 bp    mRNA            EST       18-JUN-1996
DEFINITION  me45f07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:390469 5' similar to SW:NUPM_BOVIN P42029
            NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT ;, mRNA sequence.
ACCESSION   W71856
VERSION     W71856.1  GI:1381943
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:242301
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: mob.REGA+ET
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .52
```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:390469"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
BASE COUNT 14 a 15 c 15 g 8 t
ORIGIN

Query Match 52.0%; Score 13; DB 11; Length 52;
Best Local Similarity 76.2%; Pred. No. 7.3e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 acagctcgcccccattaacat 21
|||||| | ||||| | |||
Db 23 ACAGCTGACGCCCATCATCAT 43

RESULT 5
BF643572
LOCUS BF643572 52 bp mRNA EST 20-DEC-2000
DEFINITION NF057E06EC1F1051 Elicited cell culture Medicago truncatula cDNA clone NF057E06EC 5', mRNA sequence.
ACCESSION BF643572
VERSION BF643572.1 GI:11908793
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 52)
AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 52 Std Error: 0.00
Plate: 057 row: E column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .52
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF057E06EC"
/clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
BASE COUNT 9 a 16 c 3 g 24 t
ORIGIN

Query Match 52.0%; Score 13; DB 11; Length 52;
Best Local Similarity 76.2%; Pred. No. 7.3e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ctcgcccccattaacatattc 25
||| | || || |||||| ||
Db 31 CTCTCTCCTATCAACATAATC 51

RESULT 6
TA235H01P
LOCUS TA235H01P 52 bp DNA GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 235h01, forward sequence, genomic survey sequence.
ACCESSION AL481430
VERSION AL481430.1 GI:11847124
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 52)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .52
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="235h01"
BASE COUNT 17 a 16 c 9 g 10 t
ORIGIN

Query Match 52.0%; Score 13; DB 13; Length 52;
Best Local Similarity 76.2%; Pred. No. 7.3e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ctcgcccccattaacatattc 25
| |||| | |||||||| ||
Db 19 CACGCCATCCTTAACATAATC 39

RESULT 7
AI723111
LOCUS AI723111 49 bp mRNA EST 07-JUN-2001

```
DEFINITION  fc25g02.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
            IMAGE:3722450 5' similar to SW:HIRA_FUGRU O42611 HIRA PROTEIN ;,
            mRNA sequence.
ACCESSION   AI723111
VERSION     AI723111.1  GI:5041440
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fc25g02.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:3722450"
                     /clone_lib="Zebrafish WashU MPIMG EST"
                     /sex="mixed"
                     /tissue_type="26 somite embryos, adult livers, shield
                     stage embryos"
                     /lab_host="XL1-blue MRF"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'];
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
                     Institut fuer Molekulare Genetik,Berlin). cDNAs for EST
                     analysis were selected following oligonucleotide
                     hybridization fingerprinting of arrayed clones from
                     zebrafish late somitogenesis (26 ss), adult liver or
                     embryonic shield stage (5.6 h) libraries.  Fingerprint
                     data were used to computationally cluster cDNAs, and a
                     single cDNA from each cluster was chosen for sequencing.
                     In some cases multiple members of the same cluster were
                     sequenced to assess clustering parameters or single clones
                     were sequenced additional times to assess quality
                     control."
BASE COUNT       15 a     14 c      5 g     15 t
ORIGIN


  Query Match             51.2%;  Score 12.8;  DB 10;  Length 49;
  Best Local Similarity   70.8%;  Pred. No. 8.9e+04;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatatt 24
           ||||||| || |||  | | | ||
Db       1 ACAGCTCTCCACCACAATCTTTTT 24


RESULT   8
AU107456
LOCUS       AU107456       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU107456 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HSI00655, mRNA sequence.
ACCESSION   AU107456
VERSION     AU107456.1  GI:13556977
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HSI00655"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT       12 a     14 c     14 g     10 t
ORIGIN


  Query Match             51.2%;  Score 12.8;  DB 10;  Length 50;
  Best Local Similarity   70.8%;  Pred. No. 8.9e+04;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatatt 24
           ||||| | | |  ||| || ||||
Db      14 ACAGCACACACAGATTGACCTATT 37


RESULT   9
AA190304/c
LOCUS       AA190304       52 bp    mRNA            EST       17-FEB-1997
DEFINITION  mt94h01.r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:637585
            5' similar to SW:CATD_CHICK Q05744 CATHEPSIN D PRECURSOR ;, mRNA
            sequence.
ACCESSION   AA190304
VERSION     AA190304.1  GI:1778984
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
```

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  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:389577
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:637585"
                     /clone_lib="Soares mouse 3NbMS"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
BASE COUNT       10 a     10 c     22 g     10 t
ORIGIN


  Query Match            51.2%;  Score 12.8;  DB 10;  Length 52;
  Best Local Similarity  87.5%;  Pred. No. 9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 cagctcgcccccatta 17
           |||||| ||||||| |
Db      31 CAGCTCTCCCCCATCA 16


RESULT  10
AZ662142/c
LOCUS       AZ662142       30 bp    DNA             GSS       14-DEC-2000
DEFINITION  1M0541M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0541M03 F, DNA sequence.
ACCESSION   AZ662142
VERSION     AZ662142.1  GI:11799288
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0541  row: M  column: 03
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0541M03"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       10 a      4 c      6 g     10 t
ORIGIN


  Query Match            50.4%;  Score 12.6;  DB 13;  Length 30;
  Best Local Similarity  78.9%;  Pred. No. 1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       6 tcgcccccattaacatatt 24
           | |||| |||||||  |||
Db      27 TGGCCCACATTAACTAATT 9


RESULT  11
AA857265/c
LOCUS       AA857265       49 bp    mRNA            EST       09-MAR-1998
DEFINITION  of75f01.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1436185 3'
            similar to SW:ULC6_HCMVA P16836 HYPOTHETICAL PROTEIN UL126. ;, mRNA
            sequence.
ACCESSION   AA857265
VERSION     AA857265.1  GI:2945567
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
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            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1436185"
                     /clone_lib="NCI_CGAP_Co8"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     colon adenocarcinoma, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       11 a      8 c     16 g     14 t
ORIGIN


  Query Match             50.4%;  Score 12.6;  DB 10;  Length 49;
  Best Local Similarity   78.9%;  Pred. No. 1.1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 acagctcgcccccattaac 19
          ||| | | |||||||| ||
Db     33 ACAACCCCCCCCCATTCAC 15


RESULT  12
AU102605/c
LOCUS       AU102605       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU102605 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP14573, mRNA sequence.
ACCESSION   AU102605
VERSION     AU102605.1  GI:13552126
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HEP14573"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT        5 a     18 c     18 g      9 t
ORIGIN


  Query Match             50.4%;  Score 12.6;  DB 10;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 1.1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 acagctcgcccccattaac 19
          || || || ||||| ||||
Db     25 ACGGCGCGGCCCCAGTAAC 7


RESULT  13
AU104819/c
LOCUS       AU104819       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU104819 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC03993, mRNA sequence.
ACCESSION   AU104819
VERSION     AU104819.1  GI:13554340
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HRC03993"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT        6 a     10 c     22 g     12 t
ORIGIN


  Query Match             50.4%;  Score 12.6;  DB 10;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 1.1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 gctcgccccccattaacata 22
          |||||||||||  |  || |
Db     27 GCTCGCCCCCACTCCCACA 9


RESULT  14
AZ460727/c
LOCUS       AZ460727       60 bp    DNA             GSS       04-OCT-2000
DEFINITION  1M0266011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0266011 F, DNA sequence.
ACCESSION   AZ460727
VERSION     AZ460727.1  GI:10618852
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
```

```
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0266  row: O  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0266O11"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a     16 c     23 g     15 t
ORIGIN


  Query Match             50.4%;  Score 12.6;  DB 13;  Length 60;
  Best Local Similarity   78.9%;  Pred. No. 1.1e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 gctcgccccccattaacata 22
          ||   ||||||| ||||||
Db     23 GCCGCCCCCCCATCAACATA 5


RESULT  15
AZ331596
LOCUS       AZ331596       36 bp    DNA           GSS       29-SEP-2000
DEFINITION  1M0059E08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059E08 R, DNA sequence.
ACCESSION   AZ331596
VERSION     AZ331596.1  GI:10394441
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: E  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0059E08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a      9 c      0 g     14 t
ORIGIN


  Query Match             49.6%;  Score 12.4;  DB 13;  Length 36;
  Best Local Similarity   72.7%;  Pred. No. 1.3e+05;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 acagctcgccccccattaacata 22
          ||| ||| |||   |||| |||
Db      5 ACATCTCCCCCTTTTTAATATA 26


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